

#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/901,938

DATE: 07/25/2001
TIME: 14:05:24

Input Set : A:\053884-5001.ST25.txt
Output Set: N:\CRF3\07252001\I901938.raw

ENTERED

3 <110> APPLICANT: ECONS, Michael
 4 WHITE, Kenneth
 5 STROM, Tim
 6 MEITINGER, Thomas
 8 <120> TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
 10 <130> FILE REFERENCE: 053884-5001
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/901,938
 C--> 13 <141> CURRENT FILING DATE: 2001-07-10
 15 <150> PRIOR APPLICATION NUMBER: 60/219,137
 16 <151> PRIOR FILING DATE: 2000-07-19
 18 <160> NUMBER OF SEQ ID NOS: 34
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1612
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1

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32	gcaccagcca	ctcagagcag	ggcacgtgt	tggggcccg	cctcaggctc	tgggtctgt	180
34	ccttgtcag	cgtctgcagc	atgagcgtcc	tcagagccta	tcccaatgcc	tcccactgc	240
36	tcggctccag	ctggggtggc	ctgatccacc	tgtacacagc	cacagccagg	aacagctacc	300
38	acctgcagat	ccacaagaat	ggccatgtgg	atggcgcacc	ccatcagacc	atctacagt	360
40	ccctgtatgt	cagatcagag	gatgctggct	ttgtggtgat	tacaggtgt	atgagcagaa	420
42	gatacctctg	catggatttc	agaggcaaca	tttttggatc	acactatttc	gaccggaga	480
44	actgcagggt	ccaacaccag	acgctggaaa	acgggtacga	cgtctaccac	tctcctcagt	540
46	atcaacttcct	ggtcagtcg	ggccggggcga	agagagcctt	cctgccaggc	atgaacccac	600
48	ccccgtactc	ccagttcctg	tcccggagga	acgagatccc	cctaattcac	ttcaacaccc	660
50	ccataccacg	gcccacaccc	cggagcgtcc	aggacgactc	ggagcgggac	ccccgtacg	720
52	tgctgaagcc	ccgggccccgg	atgaccccccgg	ccccggctc	ctgttcacag	gagctcccg	780
54	gcgccgagga	caacagcccg	atggccagtg	acccattagg	ggtggtcagg	ggcgtcag	840
56	tgaacacgca	cgctggggga	acggggccgg	aaggctgcc	ccccctcgcc	aagttcatct	900
58	agggtcgctg	gaagggcacc	ctcttaacc	catccctcag	caaacgcagc	tcttccaag	960
60	gaccagggtcc	cttgcacgttc	cgaggatggg	aaaggtgaca	ggggcatgt	tggaatttgc	1020
62	tgcttcctg	gggtcccttc	cacaggaggt	cctgtgagaa	ccaaccttg	aggcccaagt	1080
64	catgggtttt	caccgccttc	ctcaactccat	atagaacacc	tttccaata	ggaaacccca	1140
66	acaggttaaac	tagaaatttc	cccttcatga	agtagagag	aagggtctc	tcccaacata	1200
68	tttctttcc	ttgtgcctct	cctctttatc	acttttaagc	ataaaaaaaaaa	aaaaaaaaaa	1260
70	aaaaaaaaaa	aaaagcagt	ggttcctgag	ctcaagactt	tgaaggtgt	ggaaagagga	1320
72	aatcgagat	cccagaagct	tctccactgc	cctatgcatt	tatgttagat	gccccgatcc	1380
74	cactggcatt	tgagtgtgca	aaccttgaca	ttaacagctg	aatggggcaa	gttgatgaaa	1440
76	acactactt	caagccttcg	tttcccttg	agcatctctg	ggaaagagct	gtcaaaagac	1500
78	tgggttagg	ctggtaaaaa	cttgacagct	agacttgatg	cttgctgaaa	tgaggcagga	1560
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83	<210> SEQ ID NO:	2					
84	<211> LENGTH:	251					
85	<212> TYPE:	PRT					

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86 <213> ORGANISM: HOMO sapiens
 88 <400> SEQUENCE: 2
 90 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 91 1 5 10 15
 93 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 94 20 25 30
 96 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 97 35 40 45
 99 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 100 50 55 60
 102 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 103 65 70 75 80
 105 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 106 85 90 95
 108 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 109 100 105 110
 111 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 112 115 120 125
 114 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 115 130 135 140
 117 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 118 145 150 155 160
 120 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 121 165 170 175
 123 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 124 180 185 190
 126 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 127 195 200 205
 129 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 130 210 215 220
 132 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 133 225 230 235 240
 135 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 136 245 250
 138 <210> SEQ ID NO: 3
 139 <211> LENGTH: 1559
 140 <212> TYPE: DNA
 141 <213> ORGANISM: Mus sp.
 143 <400> SEQUENCE: 3
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 146 tagggacctg ctttagactc ctggggccg tgctctgcac tgtctgcac ttgggactg 120
 148 ctagagccta tccggacact tccccattgc ttggctccaa ctgggaagc ctgaccacc 180
 150 tttacacggc tacagccagg accagctatc acctacagat ccataggat ggtcatgtag 240
 152 atggcacccc ccatcagacc atctacagt ccctgtatgat tacatcagag gacgcccgt 300
 154 ctgtgggtat aacaggagcc atgactcgaa gtttctttg tatggatctc cacggcaaca 360
 156 tttttggatc gtttacttc agcccagaga atttcaagtt ccggcagttt acgtggaga 420
 158 atggctatga cgttacttg tcgcagaagc atcactacct ggtgagcctg ggccgcgcca 480
 160 agcgcacatctt ccagccgggc accaaccgc cggcccttc ccagttctg gctcgcagga 540
 162 acgaggtccc gctgctgcat ttctacactg ttcccccacg gcgccacacg cgcaagcg 600

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164	aggaccacc	ggagcgcgac	ccactgaacg	tgctcaagcc	gcggcccccgc	gccacgcctg	660											
166	tgcctgtatc	ctgctctcg	gagctgccga	gcgcagagga	aggtggccccc	gcagccagcg	720											
168	atcctctggg	ggtgctgcgc	agaggccgtg	gagatgctcg	cgggggcgcg	ggagggcgcgg	780											
170	atagggtgtcg	cccttccc	aggttcgct	aggccccag	gccaggctgc	gtccgcctcc	840											
172	atcctccagt	cggttcagcc	cacgttagagg	aaggactagg	gtacctcgag	gatgtctgct	900											
174	tctctccctt	ccctatgggc	ctgagagtca	cctgcgaggt	tccagccagg	caccgctatt	960											
176	cagaattaag	agccaacgg	gggaggctgg	agaggtggcg	cagacaggttc	tcagcaccca	1020											
178	caaatacctg	taattcttagc	tccagggaa	tctgtactca	cacacacaca	catccacaca	1080											
180	cacacacaca	cacatacatg	taattttaaa	tgttaatctg	attnaaagac	cccaacaggt	1140											
182	aaactagaca	cgaagctctt	tttattttat	tttactaaca	ggtaaaccag	acacttggcc	1200											
184	tttatttagcc	gggtctcttg	cctagcattt	taatcgatca	gttagcacga	ggaaagagtt	1260											
186	cacgccttga	acacaggaa	gaggccatct	ctgcagcttc	tagttactat	tctgggattc	1320											
188	acgggtgttt	gagtttgagc	accttgacct	taatgtcttc	actaggcaag	tcgaagaaag	1380											
190	acgcgcattt	cttcttttg	ggaagagctt	tggattggcg	ggaggctgac	aaggacacct	1440											
192	aaaccgaaca	catttcagag	ttcagcctcc	ctgaggaatg	attcgccaaat	gattctgtga	1500											
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207	Cys	Ser	Leu	Gly	Thr	Ala	Arg	Ala	Tyr	Pro	Asp	Thr	Ser	Pro	Leu	Leu		
208					20				25						30			
210	Gly	Ser	Asn	Trp	Gly	Ser	Leu	Thr	His	Leu	Tyr	Thr	Ala	Thr	Ala	Arg		
211					35				40						45			
213	Thr	Ser	Tyr	His	Leu	Gln	Ile	His	Arg	Asp	Gly	His	Val	Asp	Gly	Thr		
214					50				55						60			
216	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	Thr	Ser	Glu	Asp	Ala		
217		65				70				75					80			
219	Gly	Ser	Val	Val	Ile	Thr	Gly	Ala	Met	Thr	Arg	Arg	Phe	Leu	Cys	Met		
220					85				90						95			
222	Asp	Leu	His	Gly	Asn	Ile	Phe	Gly	Ser	Leu	His	Phe	Ser	Pro	Glu	Asn		
223					100				105						110			
225	Cys	Lys	Phe	Arg	Gln	Trp	Thr	Leu	Glu	Asn	Gly	Tyr	Asp	Val	Tyr	Leu		
226					115				120						125			
228	Ser	Gln	Lys	His	His	Tyr	Leu	Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ile		
229					130				135						140			
231	Phe	Gln	Pro	Gly	Thr	Asn	Pro	Pro	Phe	Ser	Gln	Phe	Leu	Ala	Arg			
232		145				150				155					160			
234	Arg	Asn	Glu	Val	Pro	Leu	Leu	His	Phe	Tyr	Thr	Val	Arg	Pro	Arg	Arg		
235					165				170						175			
237	His	Thr	Arg	Ser	Ala	Glu	Asp	Pro	Pro	Glu	Arg	Asp	Pro	Leu	Asn	Val		
238					180				185						190			
240	Leu	Lys	Pro	Arg	Pro	Arg	Ala	Thr	Pro	Val	Pro	Val	Ser	Cys	Ser	Arg		
241					195				200						205			
243	Glu	Leu	Pro	Ser	Ala	Glu	Glu	Gly	Gly	Pro	Ala	Ala	Ser	Asp	Pro	Leu		
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246 Gly Val Leu Arg Arg Gly Arg Gly Asp Ala Arg Gly Gly Ala Gly Gly
247 225 230 235 240
249 Ala Asp Arg Cys Arg Pro Phe Pro Arg Phe Val
250 245 250
252 <210> SEQ ID NO: 5
253 <211> LENGTH: 17
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <400> SEQUENCE: 5
259 Cys Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser
260 1 5 10 15
262 Asp
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 25
267 <212> TYPE: DNA
268 <213> ORGANISM: Homo sapiens
270 <400> SEQUENCE: 6
271 cgggatccac gatgttgggg gcccg 25
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 25
276 <212> TYPE: DNA
277 <213> ORGANISM: Homo sapiens
279 <400> SEQUENCE: 7
280 ggaattccta gatgaacttg gcgaa 25
283 <210> SEQ ID NO: 8
284 <211> LENGTH: 21
285 <212> TYPE: DNA
286 <213> ORGANISM: Homo sapiens
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292 <210> SEQ ID NO: 9
293 <211> LENGTH: 21
294 <212> TYPE: DNA
295 <213> ORGANISM: Homo sapiens
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301 <210> SEQ ID NO: 10
302 <211> LENGTH: 21
303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
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311 <211> LENGTH: 21
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313 <213> ORGANISM: Homo sapiens
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Input Set : A:\053884-5001.ST25.txt
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320 <211> LENGTH: 21
321 <212> TYPE: DNA
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328 <210> SEQ ID NO: 13
329 <211> LENGTH: 21
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <400> SEQUENCE: 13
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338 <211> LENGTH: 139
339 <212> TYPE: PRT
340 <213> ORGANISM: Homo Sapiens
342 <400> SEQUENCE: 14
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347 Gln Met His Pro Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asn Ser
348 20 25 30
350 Asp Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
351 35 40 45
353 Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala Met Asn Gly Glu Gly
354 50 55 60
356 Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu Cys Lys Phe Lys Glu
357 65 70 75 80
359 Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Thr Leu Tyr Arg
360 85 90 95
362 Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly
363 100 105 110
365 Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ser Ser His
366 115 120 125
368 Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr
369 130 135
371 <210> SEQ ID NO: 15
372 <211> LENGTH: 139
373 <212> TYPE: PRT
374 <213> ORGANISM: Homo Sapiens
376 <400> SEQUENCE: 15
378 Leu Lys Gly Ile Val Thr Arg Leu Tyr Cys Arg Gln Gly Tyr Tyr Leu
379 1 5 10 15
381 Gln Met His Pro Asp Gly Ala Leu Asp Gly Thr Lys Asp Asp Ser Thr
382 20 25 30
384 Asn Ser Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
385 35 40 45
387 Ile Gln Gly Val Lys Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly
388 50 55 60
390 Tyr Leu Tyr Pro Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu
391 65 70 75 80

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date